



SEQUENCE LISTING

<110> Cornell Research Foundation
Chang, Yung-Fu

<120> Ehrlichia canis genes and vaccines

<130> 1258-006 CIP

<140> 10/004,494

<141> 2001-11-02

<150> 09/358,322

<151> 1999-07-21

<160> 14

<170> PatentIn version 3.3

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<211> 5299

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<220>

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gtactataaa taagtagcat aaaacacaag taatcaaaat cgagatacta caaaaaacia	5160
cattactata ttcaaagtta tttaatatac caaaactaat tccagcattc cacactgtag	5220
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 <213> Ehrlichia canis

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 <223> Protein translated from nucleotides 12 through 533 (cytochrome oxidase homolog).

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 cta tct atg ata tgt tta gtg tac gct tct gta cca cta tat agt ata 96
 Leu Ser Met Ile Cys Leu Val Tyr Ala Ser Val Pro Leu Tyr Ser Ile
 20 25 30
 ttt tgt aaa gta aca ggt tat gga ggt aca gta aga aca agt aat ata 144
 Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser Asn Ile
 35 40 45
 tca aat tct aaa ata ggt aac act att att aaa gtc aga ttt aat gca 192
 Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe Asn Ala
 50 55 60
 gat ata cac aaa caa ctg cca tgg aaa ttc tat cca gaa gta tct cat 240
 Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val Ser His
 65 70 75 80
 gta ttt gta aaa cca gga gaa caa aaa ttg att ttc tac cgc gca gaa 288
 Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg Ala Glu
 85 90 95
 aat cta ctt gat gag gac act tca gga atg gct gta tat aat gtt aca 336
 Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn Val Thr
 100 105 110
 cca cat aaa gta gga aaa tat ttt aat aag gta gct tgt ttt tgt ttc 384
 Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe Cys Phe
 115 120 125
 acc aaa caa aca tta tac cct cat caa aaa act ata atg cca gta tca 432
 Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro Val Ser
 130 135 140
 ttt ttt ata gat cca gcc ata gaa aca gat cct gaa act gct gac gta 480
 Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala Asp Val
 145 150 155 160
 aaa ctc atc act ctt tca tat gta ttc ttt aag tac aaa gaa 522
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35 40 45

Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe Asn Ala
50 55 60

Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val Ser His
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Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg Ala Glu
85 90 95

Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn Val Thr
100 105 110

Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe Cys Phe
115 120 125

Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro Val Ser
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Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala Asp Val
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Lys Leu Ile Thr Leu Ser Tyr Val Phe Phe Lys Tyr Lys Glu
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aat gga atg gaa gta tac gtg att cca aat cat cgc gca cca gca gtc	144
Asn Gly Met Glu Val Tyr Val Ile Pro Asn His Arg Ala Pro Ala Val	
35 40 45	
atg cac atg gta tta tac aaa gtc ggt gga act gat gat cca gta gga	192
Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro Val Gly	
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Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser Gly Thr	
65 70 75 80	

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ttc Phe	aat Asn	gca Ala	agc Ser 100	aca Thr	tct Ser	caa Gln	ttt Phe	tgt Cys 105	act Thr	ata Ile	tac Tyr	tac Tyr	gaa Glu 110	tta Leu	ata Ile	336
cca Pro	aaa Lys	caa Gln 115	tat Tyr	tta Leu	tct Ser	ctt Leu	gca Ala 120	atg Met	gat Asp	att Ile	gaa Glu	tca Ser 125	gac Asp	aga Arg	atg Met	384
cag Gln	aat Asn 130	ttt Phe	aag Lys	gtt Val	acc Thr	gac Asp 135	aaa Lys	gca Ala	tta Leu	ata Ile	aga Arg 140	gaa Glu	caa Gln	aag Lys	gta Val	432
gtc Val 145	tta Leu	gaa Glu	gaa Glu	aga Arg	aaa Lys 150	atg Met	aga Arg	gtt Val	gaa Glu	agc Ser 155	caa Gln	gca Ala	aaa Lys	aac Asn	ata Ile 160	480
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gct Ala	gaa Glu	gcc Ala 195	ttt Phe	cat His	aag Lys	cta Leu	cat His 200	tat Tyr	agt Ser	cct Pro	aat Asn	aat Asn 205	gct Ala	ata Ile	tta Leu	624
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caa Gln 225	tac Tyr	tat Tyr	ggg Gly	aaa Lys	ata Ile 230	cca Pro	tct Ser	aat Asn	aat Asn	aag Lys 235	aaa Lys	cct Pro	tca Ser	agt Ser	caa Gln 240	720
gtt Val	agg Arg	gta Val	gaa Glu	cca Pro 245	ccg Pro	cat His	aaa Lys	aca Thr	aat Asn 250	atg Met	act Thr	tta Leu	aca Thr	tta Leu 255	aaa Lys	768
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ata Ile	ctc Leu 290	ggt Gly	agt Ser	ggt Gly	aaa Lys	ttc Phe 295	agc Ser	ctg Leu	ctt Leu	tac Tyr	aat Asn 300	gat Asp	ttg Leu	gta Val	att Ile	912
aac Asn 305	aat Asn	cca Pro	ata Ile	gtt Val	aca Thr 310	tcg Ser	ata Ile	aaa Lys	aca Thr	gat Asp 315	tat Tyr	aat Asn	tac Tyr	tta Leu	act Thr 320	960
gac Asp	agc Ser	gat Asp	aat Asn	tac Tyr 325	ctt Leu	tcc Ser	att Ile	gaa Glu	gct Ala 330	ata Ile	cct Pro	aaa Lys	aac Asn	ggg Gly 335	atc Ile	1008
tct Ser	aca Thr	gaa Glu	gct Ala 340	gta Val	gaa Glu	caa Gln	gaa Glu	att Ile 345	cat His	aaa Lys	tgt Cys	ata Ile	aat Asn 350	aat Asn	tat Tyr	1056
tta Leu	gaa Glu	aat Asn	gga Gly	att Ile	tca Ser	gca Ala	gaa Glu	tat Tyr	tta Leu	gaa Glu	agt Ser	gca Ala	aag Lys	tat Tyr	aaa Lys	1104

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tcc gct atg gaa aat atc ttt caa aac aat ata aga tta acc ggg cat Ser Ala Met Glu Asn Ile Phe Gln Asn Asn Ile Arg Leu Thr Gly His 420 425 430			1296
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 <213> Ehrlichia canis

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 35 40 45

Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro Val Gly
 50 55 60

Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser Gly Thr
 65 70 75 80

Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly Gly Asn
 85 90 95

Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu Leu Ile
 100 105 110

Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp Arg Met
 115 120 125

Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln Lys Val
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Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys Asn Ile
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 Pro Val Val Gly Trp Glu His Glu Ile Ser Asn Tyr Asn Lys Glu Val
 180 185 190
 Ala Glu Ala Phe His Lys Leu His Tyr Ser Pro Asn Asn Ala Ile Leu
 195 200 205
 Ile Val Thr Gly Asp Ala Asp Pro Gln Glu Val Ile Thr Leu Ala Lys
 210 215 220
 Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Lys Pro Ser Ser Gln
 225 230 235 240
 Val Arg Val Glu Pro Pro His Lys Thr Asn Met Thr Leu Thr Leu Lys
 245 250 255
 Asp Ser Ser Val Glu Ile Pro Glu Leu Phe Leu Met Tyr Gln Ile Pro
 260 265 270
 Asn Gly Ile Thr Asn Lys Asn Tyr Ile Leu Asn Met Met Leu Ala Glu
 275 280 285
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 Asn Asn Pro Ile Val Thr Ser Ile Lys Thr Asp Tyr Asn Tyr Leu Thr
 305 310 315 320
 Asp Ser Asp Asn Tyr Leu Ser Ile Glu Ala Ile Pro Lys Asn Gly Ile
 325 330 335
 Ser Thr Glu Ala Val Glu Gln Glu Ile His Lys Cys Ile Asn Asn Tyr
 340 345 350
 Leu Glu Asn Gly Ile Ser Ala Glu Tyr Leu Glu Ser Ala Lys Tyr Lys
 355 360 365
 Val Lys Ala His Leu Thr Tyr Ala Phe Asp Gly Leu Thr Phe Ile Ser
 370 375 380
 Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser Glu Ile
 385 390 395 400
 Ser Asn Ile Tyr Asp Thr Ile Asp Lys Val Ser Ile Gln Asp Val Asn
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 Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala Thr Thr
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 aaa aat aaa ata cac tat cta tat gtt gaa cat cat aac cta cca aca 144
 Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu Pro Thr
 35 40 45
 att tcc tta aaa ttt gca ttc aag aaa gca gga tac gct tat gat gcc 192
 Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr Asp Ala
 50 55 60
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 Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu Asn Glu
 65 70 75 80
 gga tca aaa aac aac tat gct ctc agt ttt gca caa caa tta gaa ggc 288
 Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu Glu Gly
 85 90 95
 aaa ggt ata gac tta aaa ttt gat ata gac cta gac aat ttt tat ata 336
 Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe Tyr Ile
 100 105 110
 tca tta aaa acc tta tca gaa aac ttt gaa gaa gcc cta gtt tta ctc 384
 Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val Leu Leu
 115 120 125
 agt gat tgc ata ttc aac acc gtc aca gat caa gaa ata ttc aat aga 432
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 ata ata gca gaa cag att gca cat gtt aaa tca tta tat tct gct cct 480
 Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser Ala Pro
 145 150 155 160
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 Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys Gly His
 165 170 175
 cca tat tct aac aaa gtt tac ggg aca tta aat aca atc aat aat atc 576
 Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn Asn Ile
 180 185 190
 aac cag gaa gac gtt gca tta tat ata aaa aat agt ttt gac aag gaa 624
 Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp Lys Glu
 195 200 205
 caa atc gtt atc agc gca gca gga gat gta gat cca aca cag cta tca 672
 Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln Leu Ser
 210 215 220

aat tta cta gat aaa tat att ctt tcc aaa ttg cca tct ggt aat aac	720
Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly Asn Asn	
225 230 235 240	
aaa aat acc ata cca gat acg act gtt aat aga gaa gac aca tta tta	768
Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr Leu Leu	
245 250 255	
tat gta cag aga gat gta cca caa agt gtc ata atg ttt gct aca gac	816
Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala Thr Asp	
260 265 270	
aca gta cca tat cac agc aaa gac tat cat gca tca aac ttg ttc aat	864
Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu Phe Asn	
275 280 285	
act atg cta ggc gga tta agt ctc aat tca ata tta atg ata gaa tta	912
Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile Glu Leu	
290 295 300	
aga gac aag tta gga tta aca tac cat agt agc agt tca cta tct aac	960
Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu Ser Asn	
305 310 315 320	
atg aat cat agt aat gtg cta ttt ggt aca ata ttc act gat aat acc	1008
Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp Asn Thr	
325 330 335	
aca gta aca aaa tgt ata tcc gtc tta aca gat att ata gag cac att	1056
Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu His Ile	
340 345 350	
aaa aag tat gga gtt gat gaa gac act ttt gca att gca aaa tct agt	1104
Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys Ser Ser	
355 360 365	
att acc aac tct ttt att tta tct atg tta aat aac aat aat gtt agt	1152
Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn Val Ser	
370 375 380	
gag ata ttg tta agc tta caa tta cac gat cta gat ccg agt tat att	1200
Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser Tyr Ile	
385 390 395 400	
aat aaa tac aat tct tac tac aaa gca ata aca ata gaa gaa gta aat	1248
Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu Val Asn	
405 410 415	
aaa att gcc aag aaa att tta tct aat gaa tta gta ata att gaa gta	1296
Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile Glu Val	
420 425 430	
gga aaa aac aat aac ata aat ggc aaa caa ata gat gct aaa aaa cac	1344
Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys Lys His	
435 440 445	
ata ctt ggt	1353
Ile Leu Gly	
450	

<210> 7
 <211> 451
 <212> PRT
 <213> Ehrlichia canis

<400> 7

Met Arg Asn Ile Leu Cys Tyr Thr Leu Ile Leu Ile Phe Phe Ser Phe

1

5

10

15

Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala Thr Thr
20 25 30

Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu Pro Thr
35 40 45

Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr Asp Ala
50 55 60

Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu Asn Glu
65 70 75 80

Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu Glu Gly
85 90 95

Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe Tyr Ile
100 105 110

Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val Leu Leu
115 120 125

Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe Asn Arg
130 135 140

Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser Ala Pro
145 150 155 160

Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys Gly His
165 170 175

Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn Asn Ile
180 185 190

Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp Lys Glu
195 200 205

Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln Leu Ser
210 215 220

Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly Asn Asn
225 230 235 240

Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr Leu Leu
245 250 255

Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala Thr Asp
260 265 270

Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu Phe Asn
275 280 285

Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile Glu Leu
 290 300

Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu Ser Asn
 305 310 315 320

Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp Asn Thr
 325 330 335

Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu His Ile
 340 345 350

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys Ser Ser
 355 360 365

Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn Val Ser
 370 375 380

Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser Tyr Ile
 385 390 395 400

Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu Val Asn
 405 410 415

Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile Glu Val
 420 425 430

Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys Lys His
 435 440 445

Ile Leu Gly
 450

<210> 8
 <211> 663
 <212> DNA
 <213> Ehrlichia canis

<220>
 <221> CDS
 <222> (1)..(663)
 <223> Protein translated from nucleotides 4,132 through 4,794 (mmpA).

<400> 8
 atg aaa gct cat agc aca agt ata cgg aac ttt cag cct tta gaa aga 48
 Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu Glu Arg
 1 5 10 15

gct gct ata atc att gca gtg tta ggt tta gct gca ttc ttg ttt gct 96
 Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu Phe Ala
 20 25 30

gct gct gcc tgc agt gat cgt ttc caa aga ttg caa tta aca aat cca 144
 Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr Asn Pro
 35 40 45

ttt gta ata gca gga atg gtt ggc ctt gca gtt ctt tta gtt gct tcc 192
 Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val Ala Ser

50	55	60	
tta aca gca gca tta agt ata tgc tta act aaa agt aag caa gtc aca Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln Val Thr 65 70 75 80			240
caa cat gct att aga cat cgc ttt gga tac gag tca agc act tct tct Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr Ser Ser 85 90 95			288
tct gta ctg ctt gca ata tca ata att tct tta tta ctt gct gca gca Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala Ala 100 105 110			336
ttt tgt gga aag ata atg ggt aat gac aac cca gat cta ttc ttt agc Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe Phe Ser 115 120 125			384
aag atg caa gaa ctc tcc aat cca ctt gtt gtt gca gct att gta gcc Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile Val Ala 130 135 140			432
gtt tct gtt ttc cta ctc tca ttc gta atg tat gct gca aag aac att Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys Asn Ile 145 150 155 160			480
ata agt cca gat aaa caa act cac gtt att ata tta tct aat caa caa Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn Gln Gln 165 170 175			528
act ata gaa gaa gca aaa gta gat caa gga atg aat att ttg tca gca Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu Ser Ala 180 185 190			576
gta ctc cca gca gct ggc att gac atc atg act ata gct tct tgt gac Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser Cys Asp 195 200 205			624
att tta gca gtg agc agc cgg gga tcc tct cag cat caa Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln 210 215 220			663

<210> 9
 <211> 221
 <212> PRT
 <213> Ehrlichia canis

<400> 9

Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu Glu Arg
1 5 10 15

Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu Phe Ala
20 25 30

Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr Asn Pro
35 40 45

Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val Ala Ser
50 55 60

Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln Val Thr
65 70 75 80

Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr Ser Ser
85 90 95

Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala Ala Ala
100 105 110

Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe Phe Ser
115 120 125

Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile Val Ala
130 135 140

Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys Asn Ile
145 150 155 160

Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn Gln Gln
165 170 175

Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu Ser Ala
180 185 190

Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser Cys Asp
195 200 205

Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln
210 215 220

<210> 10
<211> 417
<212> DNA
<213> Ehrlichia canis

<220>
<221> CDS
<222> (1)..(417)
<223> Protein translated from complementary sequence derived from
nucleotides 4,883 through 5,299 (partial lipoprotein signal
peptidase homolog).

<400> 10
gat cag gta agt aaa tgg tat gta gta aat ttg ata gga gat aaa ggt 48
Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp Lys Gly
1 5 10 15

gta ata gag ata tta agc ttc ttg cgc ttt act aca gtg tgg aat cct 96
Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp Asn Pro
20 25 30

gga att agt ttt ggt ata tta aat aac ttt gaa tat agt aat gtt gtt 144
Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn Val Val
35 40 45

ttt tgt agt atc tcg att ttg att act tgt gtt tta tgc tac tta ttt 192
Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr Leu Phe
50 55 60

ata gta cag cca cat tat aga tta cct ctt gta atc att att ggg ggg 240
Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile Gly Gly
65 70 75 80

tca ata gga aat atc ata gat aga ata aga tat ggt gct gtc tat gat	288
Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val Tyr Asp	
85 90 95	
ttt ata gat ttt tat atc aat aac tta cat tgg cct gta ttc aac ctg	336
Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe Asn Leu	
100 105 110	
gcg gat tct ttt ata ttt tta ggt ata gta ata ata atg gca aag agt	384
Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala Lys Ser	
115 120 125	
aat aac cac atg aaa caa att aac tgt aac tcc	417
Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser	
130 135	

<210> 11
 <211> 139
 <212> PRT
 <213> Ehrlichia canis

<400> 11

Asp Gln val Ser Lys Trp Tyr val val Asn Leu Ile Gly Asp Lys Gly
1 5 10 15
val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr val Trp Asn Pro
20 25 30
Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn val val
35 40 45
Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys val Leu Cys Tyr Leu Phe
50 55 60
Ile val Gln Pro His Tyr Arg Leu Pro Leu val Ile Ile Ile Gly Gly
65 70 75 80
ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala val Tyr Asp
85 90 95
Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro val Phe Asn Leu
100 105 110
Ala Asp Ser Phe Ile Phe Leu Gly Ile val Ile Ile Met Ala Lys Ser
115 120 125
Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser
130 135

<210> 12
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide

<400> 12
 aggcttggttc aggggtgaaga agaatccaac gacaaaagct t

<210> 13
<211> 41
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 13
aagcttttgt cgttggattc ttcttcaccc tgaacttgcc a

41

<210> 14
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Nonapeptide sequence VQGEESNDK from IL-1beta

<400> 14

Val Gln Gly Glu Glu Ser Asn Asp Lys
1 5